AMENDMENTS TO THE SPECIFICATION

In the specification:

Please replace the paragraph at page 38, lines 1 to 29 of the specification with the following amended paragraph:

The determination of percent identity between two sequences can be accomplished using a mathematical algorithm. A preferred, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-2268, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5877. Such an algorithm is incorporated into the BLASTN and BLASTX programs of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-410. BLAST nucleotide searches can be performed with the BLASTN program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the invention. BLAST protein searches can be performed with the BLASTP program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to a protein molecules of the invention. To obtain gapped alignments for comparison purposes, a newer version of the BLAST algorithm called Gapped BLAST can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389-3402, which is able to perform gapped local alignments for the programs BLASTN, BLASTP and BLASTX. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules. When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (*e.g.*, BLASTX and BLASTN) can be used. ~~See http://www.ncbi.nlm.nih.gov.~~ Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, (1988) *CABIOS* 4:11-17. Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Yet another useful algorithm for identifying regions of local sequence similarity and alignment is the FASTA algorithm as described in Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85:2444-2448. When using

the FASTA algorithm for comparing nucleotide or amino acid sequences, a PAM120 weight residue table can, for example, be used with a *k*-tuple value of 2.

Please replace the paragraph at page 86, lines 27 to 33 of the specification with the following amended paragraph:

Cervical tissues were collected and snap frozen in liquid nitrogen. The histology and cellular composition of tissues were confirmed before RNA extraction was performed. Total RNA was extracted from the frozen tissues using Trizol® ~~Trizol~~ Reagent (Life Technologies) followed by a secondary clean up step with Qiagen's RNeasy kit to increase RNA probe labeling efficiency (Qiagen, Valencia CA). Only RNA with a 28S/18S ribosomal RNA ratio of at least 1.0, calculated using Agilent Technologies 2100 Bioanalyzer (Palo Alto, CA), was used in this study.

Please replace the paragraph at page 92, line 27 through page 93, line 9 of the specification with the following amended paragraph:

Probes were designed by PrimerExpress™ ~~PrimerExpress~~ software (Applied Biosystems) based on the sequence of the specific genes and their related transcripts. Each target gene probe was labeled using FAM (6-carboxyfluorescein), and the 18s reference probe was labeled with a different fluorescent dye, VIC. The differential labeling of the target gene and internal reference gene thus enabled measurement in the same well. Primer and probes were checked for their sensitivity and specificity for each transcript of the specific gene. Forward and reverse primers and the probes for both 18s and the target gene were added to the TAQMAN® Universal PCR Master Mix (Applied Biosystems). Although the final concentration of primer and probe could vary, each was internally consistent within a given experiment. A typical experiment contained 100nM of forward and reverse primers plus 200nM probe for 18s and 900nM forward and reverse primers plus 250nM probe for the target gene. TAQMAN® matrix experiments were carried out on an ABI PRISM® ~~ABI PRISM~~ 7700 Sequence Detection System (Applied Biosystems).. The thermal cycler conditions were as follows: hold for 2 min at 50°C and 10 min at 95°C, followed by two-step PCR for 40 cycles of 95°C for 15 sec followed by 60°C for 1 min.